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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5
- (i) APPLICANT: Ryazanov, Alexey G.
Hait, William N.
Pavur, Karen S.
- 10
- (ii) TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE (EF-2 KINASE)
AND METHODS OF USE THEREFOR
- (iii) NUMBER OF SEQUENCES: 25
- 15
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: David A. Jackson, Esq.
(B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601
- 20
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 25
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:
- 30
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
- 35

(C) REFERENCE/DOCKET NUMBER: 601-1-078

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-487-5800

5

(B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2178 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCAGACG AAGACCTCAT CTTCCGCCTG GAAGGTGTTG ATGGCGGCCA GTCCCCCCGA	60
GCTGGCCATG ATGGTGATTC TGATGGGGAC AGCGACGATG AGGAAGGTTA CTTCATCTGC	120
30 CCCATCACGG ATGACCCAAG CTCGAACCAG AATGTCAATT CCAAGGTAA TAAGTACTAC	180
AGCAACCTAA CAAAAAGTGA GCGGTATAGC TCCAGCGGGT CCCC GGCAAA CTCCTTCCAC	240
35 TTCAAGGAAG CCTGGAAGCA CGCAATCCAG AAGGCCAAGC ACATGCCCGA CCCCTGGGCT	300
GAGTTCCACC TGGAAGATAT TGCCACCGAA CGTGCTACTC GACACAGGTA CAACGCCGTC	360

	ACCGGGGAAT GGCTGGATGA TGAAGTTCTG ATCAAGATGG CATCTCAGCC CTTCGGCCGA	420
	GGAGCAATGA GGGAGTGCTT CCGGACGAAG AAGCTCTCCA ACTTCTTGCA TGCCCAGCAG	480
5	TGGAAGGGCG CCTCCAATA CGTGGCGAAG CGCTACATCG AGCCCGTAGA CCGGGATGTG	540
	TACTTTGAGG ACGTGCGTCT ACAGATGGAG GCCAAGCTCT GGGGGGAGGA GTATAATCGG	600
	CACAAGCCCC CCAAGCAGGT GGACATCATG CAGATGTGCA TCATCGAGCT GAAGGACAGA	660
10	CCGGGCAAGC CCCTCTTCCA CCTGGAGCAC TACATCGAGG GCAAGTACAT CAAGTACAAC	720
	TCCAACCTCTG GCTTTGTCCG TGATGACAAC ATCCGACTGA CGCCGCAGGC CTTCAGCCAC	780
15	TTCACTTTTG AGCGTTCGG CCATCAGCTG ATAGTGGTGG ACATCCAGGG AGTTGGGGAT	840
	CTCTACACTG ACCCACAGAT CCACACGGAG ACGGGCACTG ACTTTGGAGA CGGCAACCTA	900
	GGTGTCCGCG GGATGGCGCT CTTCTTCTAC TCTCATGCCT GCAACCGGAT TTGCGAGAGC	960
20	ATGGGCCTTG CTCCCTTTGA CCTCTCGCCC CGGGAGAGGG ATGCAGTGAA TCAGAACACC	1020
	AAGCTGCTGC AATCAGCCAA GACCATCTTG AGAGGAACAG AGGAAAAATG TGGGAGCCCC	1080
25	CGAGTAAGGA CCCTCTCTGG GAGCCGGCCA CCCCTGCTCC GTCCCCCTTC AGAGAACTCT	1140
	GGAGACGAGA ACATGAGCGA CGTGACCTTC GACTCTCTCC CTTCTTCCCC ATCTTCGGCC	1200
	ACACCACACA GCCAGAAGCT AGACCACCTC CATTGGCCAG TGTTCAAGTGA CCTCGATAAC	1260
30	ATGGCATCCA GAGACCATGA TCATCTAGAC AACCACCGGG AGTCTGAGAA TAGTGGGGAC	1320
	AGCGGATACC CCAGTGAGAA GCGGGGTGAG CTGGATGACC CTGAGCCCCG AGAACATGGC	1380
35	CACTCATACA GTAATCGGAA GTACGAGTCT GACGAAGACA GCCTGGGCAG CTCTGGACGG	1440
	GTATGTGTAG AGAAGTGGA TCTCCTCAAC TCCTCCCGCC TCCACCTGCC GAGGGCTTCG	1500

GCCGTGGCCC TGGAAGTGCA AAGGCTTAAT GCTCTGGACC TCGAAAAGAA AATCGGGAAG 1560
 TCCATTTTGG GGAAGGTCCA TCTGGCCATG GTGCGCTACC ACGAGGGTGG GCGCTTCTGC 1620
 5 GAGAAGGGCG AGGAGTGGGA CCAGGAGTCG GCTGTCTTCC ACCTGGAGCA CGCAGCCAAC 1680
 CTGGGCGAGC TGGAGGCCAT CGTGGGCCTG GGACTCATGT ACTCGCAGTT GCCTCATCAC 1740
 ATCCTAGCCG ATGTCTCTCT GAAGGAGACA GAAGAGAACA AAACCAAAGG ATTTGATTAC 1800
 10 TTACTAAAGG CCGCTGAAGC TGGCGACAGG CAGTCCATGA TCCTAGTGGC GCGAGCTTTT 1860
 GACTCTGGCC AGAACCTCAG CCCGGACAGG TGCCAAGACT GGCTAGAGGC CCTGCACTGG 1920
 15 TACAACACTG CCCTGGAGAT GACGGACTGT GATGAGGGCG GTGAGTACGA CGGAATGCAG 1980
 GACGAGCCCC GGTACATGAT GCTGGCCAGG GAGGCAGAGA TGCTGTTCAC AGGAGGCTAC 2040
 GGGCTGGAGA AGGACCCGCA GAGATCAGGG GACTTGTATA CCCAGGCAGC AGAGGCAGCG 2100
 20 ATGGAAGCCA TGAAGGGCCG ACTGGCCAAC CAGTACTACC AAAAGGCTGA AGAGGCCTGG 2160
 GCCCAGATGG AGGAATAA 2178

25 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 amino acids
- (B) TYPE: amino acid
- 30 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Asp Glu Asp Leu Ile Phe Arg Leu Glu Gly Val Asp Gly Gly
 1 5 10 15

Gln Ser Pro Arg Ala Gly His Asp Gly Asp Ser Asp Gly Asp Ser Asp
 20 25 30

Asp Glu Glu Gly Tyr Phe Ile Cys Pro Ile Thr Asp Asp Pro Ser Ser
 35 40 45

Asn Gln Asn Val Asn Ser Lys Val Asn Lys Tyr Tyr Ser Asn Leu Thr
 50 55 60

Lys Ser Glu Arg Tyr Ser Ser Ser Gly Ser Pro Ala Asn Ser Phe His
 20 65 70 75 80

Phe Lys Glu Ala Trp Lys His Ala Ile Gln Lys Ala Lys His Met Pro
 85 90 95

Asp Pro Trp Ala Glu Phe His Leu Glu Asp Ile Ala Thr Glu Arg Ala
 100 105 110

Thr Arg His Arg Tyr Asn Ala Val Thr Gly Glu Trp Leu Asp Asp Glu
 115 120 125

Val Leu Ile Lys Met Ala Ser Gln Pro Phe Gly Arg Gly Ala Met Arg
 130 135 140

Glu Cys Phe Arg Thr Lys Lys Leu Ser Asn Phe Leu His Ala Gln Gln
 35 145 150 155 160

Trp Lys Gly Ala Ser Asn Tyr Val Ala Lys Arg Tyr Ile Glu Pro Val

165

170

175

Asp Arg Asp Val Tyr Phe Glu Asp Val Arg Leu Gln Met Glu Ala Lys
 180 185 190

5

Leu Trp Gly Glu Glu Tyr Asn Arg His Lys Pro Pro Lys Gln Val Asp
 195 200 205

10

Ile Met Gln Met Cys Ile Ile Glu Leu Lys Asp Arg Pro Gly Lys Pro
 210 215 220

Leu Phe His Leu Glu His Tyr Ile Glu Gly Lys Tyr Ile Lys Tyr Asn
 225 230 235 240

15

Ser Asn Ser Gly Phe Val Arg Asp Asp Asn Ile Arg Leu Thr Pro Gln
 245 250 255

Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His Gln Leu Ile Val
 260 265 270

20

Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp Pro Gln Ile His
 275 280 285

25

Thr Glu Thr Gly Thr Asp Phe Gly Asp Gly Asn Leu Gly Val Arg Gly
 290 295 300

Met Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg Ile Cys Glu Ser
 305 310 315 320

30

Met Gly Leu Ala Pro Phe Asp Leu Ser Pro Arg Glu Arg Asp Ala Val
 325 330 335

Asn Gln Asn Thr Lys Leu Leu Gln Ser Ala Lys Thr Ile Leu Arg Gly
 340 345 350

35

Thr Glu Glu Lys Cys Gly Ser Pro Arg Val Arg Thr Leu Ser Gly Ser
 355 360 365

Arg Pro Pro Leu Leu Arg Pro Leu Ser Glu Asn Ser Gly Asp Glu Asn
 370 375 380

5 Met Ser Asp Val Thr Phe Asp Ser Leu Pro Ser Ser Pro Ser Ser Ala
 385 390 395 400

Thr Pro His Ser Gln Lys Leu Asp His Leu His Trp Pro Val Phe Ser
 405 410 415

10 Asp Leu Asp Asn Met Ala Ser Arg Asp His Asp His Leu Asp Asn His
 420 425 430

Arg Glu Ser Glu Asn Ser Gly Asp Ser Gly Tyr Pro Ser Glu Lys Arg
 435 440 445

15 Gly Glu Leu Asp Asp Pro Glu Pro Arg Glu His Gly His Ser Tyr Ser
 450 455 460

20 Asn Arg Lys Tyr Glu Ser Asp Glu Asp Ser Leu Gly Ser Ser Gly Arg
 465 470 475 480

Val Cys Val Glu Lys Trp Asn Leu Leu Asn Ser Ser Arg Leu His Leu
 485 490 495

25 Pro Arg Ala Ser Ala Val-Ala Leu Glu Val Gln Arg Leu Asn Ala Leu
 500 505 510

Asp Leu Glu Lys Lys Ile Gly Lys Ser Ile Leu Gly Lys Val His Leu
 515 520 525

30 Ala Met Val Arg Tyr His Glu Gly Gly Arg Phe Cys Glu Lys Gly Glu
 530 535 540

35 Glu Trp Asp Gln Glu Ser Ala Val Phe His Leu Glu His Ala Ala Asn
 545 550 555 560

Leu Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu Met Tyr Ser Gln

565

570

575

5 Leu Pro His His Ile Leu Ala Asp Val Ser Leu Lys Glu Thr Glu Glu
 580 585 590
 Asn Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala Ala Glu Ala Gly
 595 600 605
 10 Asp Arg Gln Ser Met Ile Leu Val Ala Arg Ala Phe Asp Ser Gly Gln
 610 615 620
 Asn Leu Ser Pro Asp Arg Cys Gln Asp Trp Leu Glu Ala Leu His Trp
 625 630 635 640
 15 Tyr Asn Thr Ala Leu Glu Met Thr Asp Cys Asp Glu Gly Gly Glu Tyr
 645 650 655
 Asp Gly Met Gln Asp Glu Pro Arg Tyr Met Met Leu Ala Arg Glu Ala
 660 665 670
 20 Glu Met Leu Phe Thr Gly Gly Tyr Gly Leu Glu Lys Asp Pro Gln Arg
 675 680 685
 Ser Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala Met Glu Ala Met
 25 690 695 700
 Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys Ala Glu Glu Ala Trp
 705 710 715 720
 30 Ala Gln Met Glu Glu
 725

(2) INFORMATION FOR SEQ ID NO:3:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2175 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15 ATGGCAGACG AAGACCTCAT CTTCTGCCTG GAAGGTGTTG ACGGTGGCAG GTGCTCCCGA 60
GCTGGCCACA ATGCGGACTC TGACACAGAC AGTGACGATG ATGAGGGCTA TTTCATCTGC 120
CCCATCACTG ATGACCACAT GTCCAATCAG AATGTCAGCT CCAAAGTCCA GAGCTACTAT 180
20 AGCAACCTAA CAAAAACAGA GTGCGGCTCC ACAGGGTCAC CAGCCAGCTC CTTCCACTTC 240
AAGGAAGCCT GGAAGCATGC GATCGAGAAA GCCAAGCACA TGCCTGACCC CTGGGCTGAA 300
25 TTCCATCTCG AGGACATCGC CACAGAACAT GCTACTCGGC ACAGGTACAA CGCTGTCACC 360
GGGGAATGGC TGAAAGACGA GGTTCCTGATC AAGATGGCGT CTCAGCCCTT CGGCCGTGGA 420
GCAATGAGGG AGTGCTTCAG GACGAAGAAA CTCTCCAAC TCTTGACGC CCAGCAATGG 480
30 AAGGGGGCCT CCAACTACGT GGCCAAGCGC TACATCGAGC CGGTGGACAG GAGCGTGTAC 540
TTTGAGGATG TGCAGCTCCA GATGGAGGCG AAGCTCTGGG GGGAGGATTA CAATCGGCAC 600
35 AAGCCCCCA AGCAGGTGGA TATCATGCAG ATGTGCATCA TTGAGCTAAA GGACAGACCA 660
GGCCAGCCCC TCTTCCACTT GGAGCACTAC ATTGAGGGCA AGTACATCAA GTACAATTCC 720

AACTCAGGCT TTGTCCGTGA TGACAACATC CGACTAACCC CACAGGCCTT CAGCCATTTTC 780

ACATTTGAGC GTTCTGGTCA TCAGCTGATT GTAGTGGACA TCCAGGGTGT GGGTGACCTT 840

5 TATACCGACC CACAGATCCA CACTGAGAAA GGCCTGACT TTGGAGATGG TAACCTTGGT 900

GTCCGGGGAA TGGCTCTCTT CTTCTACTCT CATGCCTGCA ACCGGATTTG TCAGAGCATG 960

GGCCTTACGC CCTTTGACCT CTCCCCACGG GAACAGGATG CGGTGAATCA GAGCACCAGG 1020

10 CTATTGCAAT CAGCCAAGAC CATCTTGAGG GGGACAGAGG AGAAGTGTGG GAGTCCCCGC 1080

ATAAGGACAC TCTCTAGCAG CCGGCCCCCT TTGCTCCTTC GCCTGTCAGA GAACTCCGGG 1140

15 GATGAGAACA TGAGTGACGT GACCTTTGAC TCTCTGCCTT CCTCCCCGTC TTCAGCTACA 1200

CCACACAGCC AGAAACTGGA CCACCTCCAT TGGCCAGTGT TTGGTGACCT CGATAACATG 1260

GGCCCTAGAG ACCATGACCG TATGGACAAT CACCGGGACT CTGAGAATAG TGGGGACAGT 1320

20 GGGTATCCAA GCGAGAAGCG AAGTGACCTG GATGATCCTG AGCCCCGAGA ACACGGCCAC 1380

TCCAACGGCA ACCGAAGGCA TGAATCTGAC GAGGATAGCC TGGGCAGCTC TGGACGGGTC 1440

25 TGTGTGGAGA CGTGGAACCT GCTCAATCCC TCCCGCCTGC ACCTGCCGAG GCCCTCGGCC 1500

GTGGCCCTAG AAGTGCAGAG GCTAAATGCC CTGGACCTTG GAAGGAAAAT CGGGAAGTCT 1560

GTTTTGGGGA AAGTCCATTT GGCCATGGTG CGATACCACG AGGGCGGGCG CTTCTGCGAG 1620

30 AAGGATGAGG AGTGGGATCG AGAGTCAGCC ATCTTCCATC TGGAGCATGC AGCTGACCTG 1680

GGAGAACTGG AGGCCATCGT GGGCCTAGGC CTCATGTACT CTCAGCTGCC CCACCACATC 1740

35 CTGGCTGATG TCTCTCTGAA GGAGACAGAG GAGAACAAGA CAAAAGGCTT TGATTACTTA 1800

CTGAAGGCGG CAGAAGCTGG TGACAGGCAT TCCATGATTT TAGTGGCCCCG AGCTTTTGAC 1860

TCAGCTGATT

ACTGGCCTGA ACCTCAGCCC AGACAGGTGT CAAGACTGGT CGGAAGCCTT GCACTGGTAC 1920
 AACACAGCCC TGGAGACAAC AGACTGCGAT GAAGGCGGGG AGTACGATGG GATACAGGAC 1980
 5 GAGCCCCAGT ACGCACTGCT GGCCAGGGAG GCGGAGATGC TGCTACCGG GGGATTTGGA 2040
 CTGGACAAGA ACCCCCCAAG ATCAGGAGAT TTGTACACCC AGGCAGCTGA GGCAGCAATG 2100
 GAAGCCATGA AGGGCCGGCT AGCCAACCAG TACTACGAGA AGGCGGAAGA GGCCTGGGCC 2160
 10 CAGATGGAGG AATAA 2175

(2) INFORMATION FOR SEQ ID NO:4:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 724 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

- 25 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Mus musculus

- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Asp Glu Asp Leu Ile Phe Cys Leu Glu Gly Val Asp Gly Gly
 1 5 10 15

35 Arg Cys Ser Arg Ala Gly His Asn Ala Asp Ser Asp Thr Asp Ser Asp
 20 25 30

Asp Asp Glu Gly Tyr Phe Ile Cys Pro Ile Thr Asp Asp His Met Ser
 35 40 45

5 Asn Gln Asn Val Ser Ser Lys Val Gln Ser Tyr Tyr Ser Asn Leu Thr
 50 55 60

Lys Thr Glu Cys Gly Ser Thr Gly Ser Pro Ala Ser Ser Phe His Phe
 65 70 75 80

10 Lys Glu Ala Trp Lys His Ala Ile Glu Lys Ala Lys His Met Pro Asp
 85 90 95

Pro Trp Ala Glu Phe His Leu Glu Asp Ile Ala Thr Glu His Ala Thr
 100 105 110

15 Arg His Arg Tyr Asn Ala Val Thr Gly Glu Trp Leu Lys Asp Glu Val
 115 120 125

20 Leu Ile Lys Met Ala Ser Gln Pro Phe Gly Arg Gly Ala Met Arg Glu
 130 135 140

Cys Phe Arg Thr Lys Lys Leu Ser Asn Phe Leu His Ala Gln Gln Trp
 145 150 155 160

25 Lys Gly Ala Ser Asn Tyr Val Ala Lys Arg Tyr Ile Glu Pro Val Asp
 165 170 175

Arg Ser Val Tyr Phe Glu Asp Val Gln Leu Gln Met Glu Ala Lys Leu
 180 185 190

30 Trp Gly Glu Asp Tyr Asn Arg His Lys Pro Pro Lys Gln Val Asp Ile
 195 200 205

35 Met Gln Met Cys Ile Ile Glu Leu Lys Asp Arg Pro Gly Gln Pro Leu
 210 215 220

Phe His Leu Glu His Tyr Ile Glu Gly Lys Tyr Ile Lys Tyr Asn Ser

	225		230		235		240
	Asn Ser Gly Phe Val Arg Asp Asp Asn Ile Arg Leu Thr Pro Gln Ala						
		245		250		255	
5	Phe Ser His Phe Thr Phe Glu Arg Ser Gly His Gln Leu Ile Val Val						
		260		265		270	
	Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp Pro Gln Ile His Thr						
10		275		280		285	
	Glu Lys Gly Thr Asp Phe Gly Asp Gly Asn Leu Gly Val Arg Gly Met						
		290		295		300	
15	Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg Ile Cys Gln Ser Met						
		305		310		315	320
	Gly Leu Thr Pro Phe Asp Leu Ser Pro Arg Glu Gln Asp Ala Val Asn						
			325		330		335
20	Gln Ser Thr Arg Leu Leu Gln Ser Ala Lys Thr Ile Leu Arg Gly Thr						
		340		345		350	
	Glu Glu Lys Cys Gly Ser Pro Arg Ile Arg Thr Leu Ser Ser Ser Arg						
25		355		360		365	
	Pro Pro Leu Leu Leu Arg Leu Ser Glu Asn Ser Gly Asp Glu Asn Met						
		370		375		380	
30	Ser Asp Val Thr Phe Asp Ser Leu Pro Ser Ser Pro Ser Ser Ala Thr						
		385		390		395	400
	Pro His Ser Gln Lys Leu Asp His Leu His Trp Pro Val Phe Gly Asp						
		405		410		415	
35	Leu Asp Asn Met Gly Pro Arg Asp His Asp Arg Met Asp Asn His Arg						
		420		425		430	

Asp Ser Glu Asn Ser Gly Asp Ser Gly Tyr Pro Ser Glu Lys Arg Ser
 435 440 445

5 Asp Leu Asp Asp Pro Glu Pro Arg Glu His Gly His Ser Asn Gly Asn
 450 455 460

Arg Arg His Glu Ser Asp Glu Asp Ser Leu Gly Ser Ser Gly Arg Val
 465 470 475 480

10 Cys Val Glu Thr Trp Asn Leu Leu Asn Pro Ser Arg Leu His Leu Pro
 485 490 495

Arg Pro Ser Ala Val Ala Leu Glu Val Gln Arg Leu Asn Ala Leu Asp
 500 505 510

15 Leu Gly Arg Lys Ile Gly Lys Ser Val Leu Gly Lys Val His Leu Ala
 515 520 525

20 Met Val Arg Tyr His Glu Gly Gly Arg Phe Cys Glu Lys Asp Glu Glu
 530 535 540

Trp Asp Arg Glu Ser Ala Ile Phe His Leu Glu His Ala Ala Asp Leu
 545 550 555 560

25 Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu Met Tyr Ser Gln Leu
 565 570 575

Pro His His Ile Leu Ala Asp Val Ser Leu Lys Glu Thr Glu Glu Asn
 580 585 590

30 Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala Ala Glu Ala Gly Asp
 595 600 605

35 Arg His Ser Met Ile Leu Val Ala Arg Ala Phe Asp Thr Gly Leu Asn
 610 615 620

Leu Ser Pro Asp Arg Cys Gln Asp Trp Ser Glu Ala Leu His Trp Tyr

TEBET "E044660"

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(i) SEQUENCE CHARACTERISTICS:

- 25

30

(vi) ORIGINAL SOURCE:

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	ATGTTTAATA TAAAAAAGAG AAAAGAGAGT ATAACAGGTA TACCACCAAT AAATGTTAAT	60
5	AGTCCACAAT CAGTTCCATT GAGTGGAACA TTGCAATCAC CATTGATTAC ACCAAATTCA	120
	CCAAATTTTG TTTCACGTCA ATGTCCATTC AAAAAGTTTG GATGTAGTAG TTTTGTAGTT	180
10	TCAAAGGCAG AGTTTGATAA TCACTTAAAG GATGACGCAC AATTTCAATT ACAATTGGCA	240
	GTGGAGAAAT TTGATCATCA ATTTGATTTA CACACACAAT TGATGGCACA TTTTACTGAG	300
	CAAATGGAGG ATCAATTAGA GAAAACAATG AAGGTCGTAC GTAATCATAC AGATAGTTTA	360
15	GGCGGTAATG TTCAAACCAA ATTGGATGAA GGCATTGAAA AATGTATGGC TTTTGCTAAA	420
	AAGGTTGAAC AACAACAACA ACAATTGGCC AAAAGATTAA TCACTCAACA AATTCAAGAG	480
20	AAGAAATCAA CCTCTTCACC TTTAGTTAAA GGTGGTATTA GTGGTGGTGG TGGTAGTGGT	540
	GGCGATGATT CTTTGTATGG CGCAAATATA TCATCAATGT CAACTAGTAA ACAAGAATTA	600
	CAACAAGAAT TACAATCATT ATCAATTAAA ATGAAAAAAG AATTGACAGA ATTATCCGAT	660
25	GAACTATCAC AAAAATTAGA ACGTTCAACA GGTAATATAG ATATTAAAT AAAGAGAATC	720
	GAAGGTGAAG TTAATGAAAA GATTGATAAA CGTCAATTGG TCTCTACGAT CGATGATTCA	780
30	ATTGGAAAGA AAACAGATTC CATCGTTAT ACATTGGAGA GTTCAATCAT TAAAAAGGTT	840
	GAAGAGAAAG AGAAAAAGAA ATCCGAACAA AATCAACTTC TCTTTGATTC AAAGATTGAA	900
	TCCTTAAAG ATAAGATTAA AATCATTGAA ACTCAACAAT TGGATACTTC ATCAGAGGTT	960
35	AGAAAATTGA AATTAGAAAG TACAAGTAGT GGAAATTTAA TGGCAGGTCT TAATGGTACC	1020
	TCTGGTAGAC CTTATCATC TTCTCACTTT ATTCCATCCT CTGTTTCTGC CGCTGCTAAC	1080

AATATCAACA AGAATGAAAT CATGGAAGAG GTTAAAAAGG TAGAAGAGAA ACTTCAAAAG 1140
 AAAATTCGTG AAGAGATTGA TAATACAAAA GCTGAACTCT CAAAGGTTGA ACGTTCCGTT 1200
 5 AAAGATAATC GTAGTGAAAT TGAAGGTTTG GAAAAAGATT GTAAGAATCA ATTCGATAAA 1260
 CAAGACAATA AGATCAAACA AGTTGAGGAT GATTTGAAAA AGAGTGATTC ATTACTTTTG 1320
 TTAATGCAAA ATAACCTCAA GAAATATAAT GAATTTGTTG ATAGAGAACG TGATCGTGAA 1380
 10 AGTGAACGTT TGAAACTTCA AGATTCTATC AAACGTTTAG AACAAAATCA AAAGAAAATC 1440
 GAAGCTGAAA TTCAAGAAGG TAATGAACAA GTTGAACGTG TTTTACGTGA GGAAGCTTCA 1500
 15 ATCTCACCAA TTAGTTCAGT TCCAAAATCA CCAATCACAA CCAAACGTTT ATCGATTATT 1560
 TTAAATTCAC CACCAATGAC TTCACAACAA TCATCACCAA AGATTCAAGA TCTTCTCTCA 1620
 AGTAGTGGTA GTAGTAGTGT TAGTGGTATA AATATTTCTT CTGAAACCGG TGAAATGGGT 1680
 20 ATTCTTTGGG AATTTGATCC AATCATTAAC AAATGGATTA GATTATCAAT GAAGCTAAAG 1740
 GTAGAAAGAA AACCATTTGC AGAGGGTGCT CTTAGAGAGG CTTATCATAC CGTTTCATTG 1800
 25 GGTGTTGGAA CCGATGAAAA TTATCCATTA GGTACAACCA CCAAATTATT CCCACCAATT 1860
 GAAATGATTT CACCAATTTT AAAGAATAAT GAGGCAATGA CTCAATTGAA GAATGGTACA 1920
 AAATTTGTTT TGAAACTCTA CAAAAAGGAA GCTGAACAAC AAGCTAGCAG AGAATTATAC 1980
 30 TTTGAAGATG TTAAATGCA AATGGTCTGT AGAGATTGGG GTAATAAATT CAATCAAAAG 2040
 AAACCACCAA AGAAAATTGA ATTCCTTATG TCTTGGGTTG TAGAGTTAAT CGATAGATCT 2100
 35 CCTTCTTCCA ATGGTCAACC AATACTTTGT TCCATTGAAC CATTATTGGT TGGTGAATTC 2160
 AAAAAGAATA ATTCAAATTA TGGTGCAGTT TTAACCAATC GTTCAACTCC ACAAGCATTC 2220

	TCTCATTTC	CCTATGA	ACTCTCAA	AATAAA	CAAATG	ATCG	TTGTCG	GATAT	TCAAGG	TGTT	2280
	GATGATCTTT	ACACTG	ATCC	TCAAAT	TCAT	ACACCC	GATG	GTAAAG	GATT	TGGTCTTGGT	2340
5	AATCTTGGTA	AAGCAG	GTAT	CAATAA	ATTC	ATCACC	ACTC	ACAAAT	GTAA	TGCTGTTTGT	2400
	GCTCTTTTAG	ATTTAG	ATGT	TAAATT	TGGG	GGTGT	ACTAT	CTGGAA	AATA	TAAGAAACAA	2460
	CTTCAACAAG	GTACTA	TGGT	TATGCC	CAGAT	ATTCT	CCCAG	AACTTA	TGCC	ATCTGATAAC	2520
10	ACCATTAAG	TGGGTG	CAAA	ACAACT	TCCA	AAAGCT	GAA	TCTCAA	AGAA	AGATCTCAAA	2580
	TGTGTTAGCA	CCATTCA	AAG	TTTCCG	TGAA	CGTGTT	AACT	CGATCG	CATT	CTTTGATAAT	2640
15	CAAAAGTTAT	TATGCG	CTGG	TTATGG	TGAT	GGTACC	TATA	GAGTTTT	TCGA	TGTCAATGAC	2700
	AATTGGAAAT	GTTTATA	CAC	TGTCAAT	GGT	CATAGAA	AAT	CAATTG	AAAG	TATCGCTTGT	2760
	AATAGTAATT	ACATTTT	CAC	TTCATC	ACCT	GATAAC	ACCA	TCAAAG	TTCA	TATCATTCGT	2820
20	AGTGGTAACA	CCAAAT	GTAT	AGAGAC	ATTG	GTTGGT	CACA	CTGGTGA	AGT	TAATTGTGTC	2880
	GTGGCCAATG	AAAAAT	ATCT	TTTCAG	TTGT	AGTTAT	GATA	AACTAT	CAA	GGTTTGGGAT	2940
25	TTGTCAACCT	TTAAAG	AAAT	TAAATC	ATT	GAGGGT	GTTC	ATACAA	AGTA	CATTAAAACA	3000
	TTGGCTTTGA	GTGGAC	GTTA	TCTTTTT	TAGT	GGTGGT	AACG	ATCAAAT	CAT	TTACGTTTGG	3060
	GATACTGAAA	CACTTAG	TAT	GCTTTT	CAAT	ATGCAAG	GTC	ATGAAG	ATTG	GGTACTCTCT	3120
30	CTTCATTGTA	CCGCTA	GTTA	TCTTTT	CTCA	ACCTCAA	AAAG	ATAATG	TCAT	CAAGATTTGG	3180
	GATCTCTCAA	ATTTCA	GTTG	TATCGA	TACT	CTAAAAG	GTC	ATTGGA	ATTC	TGTCTCAAGT	3240
35	TGTGTCGTAA	AAGATC	GTTA	TCTATA	CAGT	GGTCTG	AAG	ATAATT	CAAT	CAAAGTTTGG	3300
	GATCTCGATA	CACTTGA	ATG	TGTTTA	CACC	ATTCCAAA	AAT	CTCATT	CTTT	GGGTGTAAAA	3360

TGTTTAATGG TTTTCAATAA TCAAATCATT TCTGCTGCTT TCGATGGTTC AATTAAAGTT 3420

TGGGAATGGC AATCGAAATA ATCTTTGTAA ATTTTGTGA AAAAA 3465

5 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Dictyostelium discoideum

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

25 Met Phe Asn Ile Lys Lys Arg Lys Glu Ser Ile Thr Gly Ile Pro Pro
1 5 10 15

Ile Asn Val Asn Ser Pro Gln Ser Val Pro Leu Ser Gly Thr Leu Gln
20 25 30

30 Ser Pro Leu Ile Thr Pro Asn Ser Pro Asn Phe Val Ser Arg Gln Cys
35 40 45

Pro Phe Lys Lys Phe Gly Cys Ser Ser Phe Leu Val Ser Lys Ala Glu
50 55 60

35 Phe Asp Asn His Leu Lys Asp Asp Ala Gln Phe His Leu Gln Leu Ala
65 70 75 80

Val Glu Lys Phe Asp His Gln Phe Asp Leu His Thr Gln Leu Met Ala
 85 90 95
 5 His Phe Thr Glu Gln Met Glu Asp Gln Leu Glu Lys Thr Met Lys Val
 100 105 110
 Val Arg Asn His Thr Asp Ser Leu Gly Gly Asn Val Gln Thr Lys Leu
 115 120 125
 10 Asp Glu Gly Ile Glu Lys Cys Met Ala Phe Ala Lys Lys Val Glu Gln
 130 135 140
 Gln Gln Gln Gln Leu Ala Lys Arg Leu Ile Thr Gln Gln Ile Gln Glu
 145 150 155 160
 15 Lys Lys Ser Thr Ser Ser Pro Leu Val Lys Gly Gly Ile Ser Gly Gly
 165 170 175
 Gly Gly Ser Gly Gly Asp Asp Ser Phe Asp Gly Ala Asn Ile Ser Ser
 180 185 190
 20 Met Ser Thr Ser Lys Gln Glu Leu Gln Gln Glu Leu Gln Ser Leu Ser
 195 200 205
 25 Ile Lys Met Lys Lys Glu Leu Thr Glu Leu Ser Asp Glu Leu Ser Gln
 210 215 220
 Lys Leu Glu Arg Ser Thr Gly Asn Ile Asp Ile Lys Ile Lys Arg Ile
 225 230 235 240
 30 Glu Gly Glu Val Asn Glu Lys Ile Asp Lys Arg Gln Leu Val Ser Thr
 245 250 255
 35 Ile Asp Asp Ser Ile Gly Lys Lys Thr Asp Ser Ile Gly Tyr Thr Leu
 260 265 270
 Glu Ser Ser Ile Ile Lys Lys Val Glu Glu Lys Glu Lys Lys Lys Ser

275

280

285

5

Glu Gln Asn Gln Leu Leu Phe Asp Ser Lys Ile Glu Ser Leu Lys Asp
 290 295 300

Lys Ile Lys Ile Ile Glu Thr Gln Gln Leu Asp Thr Ser Ser Glu Val
 305 310 315 320

10

Arg Lys Leu Lys Leu Glu Ser Thr Ser Ser Gly Asn Leu Met Ala Gly
 325 330 335

Leu Asn Gly Thr Ser Gly Arg Pro Ser Ser Ser Ser His Phe Ile Pro
 340 345 350

15

Ser Ser Val Ser Ala Ala Ala Asn Asn Ile Asn Lys Asn Glu Ile Met
 355 360 365

Glu Glu Val Lys Lys Val Glu Glu Lys Leu Gln Lys Lys Ile Arg Glu
 370 375 380

20

Glu Ile Asp Asn Thr Lys Ala Glu Leu Ser Lys Val Glu Arg Ser Val
 385 390 395 400

25

Lys Asp Asn Arg Ser Glu Ile Glu Gly Leu Glu Lys Asp Cys Lys Asn
 405 410 415

Gln Phe Asp Lys Gln Asp Asn Lys Ile Lys Gln Val Glu Asp Asp Leu
 420 425 430

30

Lys Lys Ser Asp Ser Leu Leu Leu Leu Met Gln Asn Asn Leu Lys Lys
 435 440 445

Tyr Asn Glu Phe Val Asp Arg Glu Arg Asp Arg Glu Ser Glu Arg Leu
 450 455 460

35

Lys Leu Gln Asp Ser Ile Lys Arg Leu Glu Gln Asn Gln Lys Lys Ile
 465 470 475 480

Glu Ala Glu Ile Gln Glu Gly Asn Glu Gln Val Glu Arg Val Leu Arg
 485 490 495

5 Glu Glu Ala Ser Ile Ser Pro Ile Ser Ser Val Pro Lys Ser Pro Ile
 500 505 510

Thr Thr Lys Arg Ser Ser Ile Ile Leu Asn Ser Pro Pro Met Thr Ser
 515 520 525

10 Gln Gln Ser Ser Pro Lys Ile Gln Asp Leu Leu Ser Ser Ser Gly Ser
 530 535 540

15 Ser Ser Val Ser Gly Ile Asn Ile Ser Ser Glu Thr Gly Glu Met Gly
 545 550 555 560

Ile Leu Trp Glu Phe Asp Pro Ile Ile Asn Lys Trp Ile Arg Leu Ser
 565 570 575

20 Met Lys Leu Lys Val Glu Arg Lys Pro Phe Ala Glu Gly Ala Leu Arg
 580 585 590

Glu Ala Tyr His Thr Val Ser Leu Gly Val Gly Thr Asp Glu Asn Tyr
 595 600 605

25 Pro Leu Gly Thr Thr Thr-Lys Leu Phe Pro Pro Ile Glu Met Ile Ser
 610 615 620

30 Pro Ile Ser Lys Asn Asn Glu Ala Met Thr Gln Leu Lys Asn Gly Thr
 625 630 635 640

Lys Phe Val Leu Lys Leu Tyr Lys Lys Glu Ala Glu Gln Gln Ala Ser
 645 650 655

35 Arg Glu Leu Tyr Phe Glu Asp Val Lys Met Gln Met Val Cys Arg Asp
 660 665 670

Trp Gly Asn Lys Phe Asn Gln Lys Lys Pro Pro Lys Lys Ile Glu Phe

675

680

685

5

Leu Met Ser Trp Val Val Glu Leu Ile Asp Arg Ser Pro Ser Ser Asn
 690 695 700

Gly Gln Pro Ile Leu Cys Ser Ile Glu Pro Leu Leu Val Gly Glu Phe
 705 710 715 720

10

Lys Lys Asn Asn Ser Asn Tyr Gly Ala Val Leu Thr Asn Arg Ser Thr
 725 730 735

Pro Gln Ala Phe Ser His Phe Thr Tyr Glu Leu Ser Asn Lys Gln Met
 740 745 750

15

Ile Val Val Asp Ile Gln Gly Val Asp Asp Leu Tyr Thr Asp Pro Gln
 755 760 765

Ile His Thr Pro Asp Gly Lys Gly Phe Gly Leu Gly Asn Leu Gly Lys
 770 775 780

20

Ala Gly Ile Asn Lys Phe Ile Thr Thr His Lys Cys Asn Ala Val Cys
 785 790 795 800

25

Ala Leu Leu Asp Leu Asp Val Lys Leu Gly Gly Val Leu Ser Gly Asn
 805 810 815

Asn Lys Lys Gln Leu Gln Gln Gly Thr Met Val Met Pro Asp Ile Leu
 820 825 830

30

Pro Glu Leu Met Pro Ser Asp Asn Thr Ile Lys Val Gly Ala Lys Gln
 835 840 845

Leu Pro Lys Ala Glu Phe Ser Lys Lys Asp Leu Lys Cys Val Ser Thr
 850 855 860

35

Ile Gln Ser Phe Arg Glu Arg Val Asn Ser Ile Ala Phe Phe Asp Asn
 865 870 875 880

Gln Lys Leu Leu Cys Ala Gly Tyr Gly Asp Gly Thr Tyr Arg Val Phe
 885 890 895

5 Asp Val Asn Asp Asn Trp Lys Cys Leu Tyr Thr Val Asn Gly His Arg
 900 905 910

Lys Ser Ile Glu Ser Ile Ala Cys Asn Ser Asn Tyr Ile Phe Thr Ser
 915 920 925

10 Ser Pro Asp Asn Thr Ile Lys Val His Ile Ile Arg Ser Gly Asn Thr
 930 935 940

Lys Cys Ile Glu Thr Leu Val Gly His Thr Gly Glu Val Asn Cys Val
 945 950 955 960

15 Val Ala Asn Glu Lys Tyr Leu Phe Ser Cys Ser Tyr Asp Lys Thr Ile
 965 970 975

20 Lys Val Trp Asp Leu Ser Thr Phe Lys Glu Ile Lys Ser Phe Glu Gly
 980 985 990

Val His Thr Lys Tyr Ile Lys Thr Leu Ala Leu Ser Gly Arg Tyr Leu
 995 1000 1005

25 Phe Ser Gly Gly Asn Asp-Gln Ile Ile Tyr Val Trp Asp Thr Glu Thr
 1010 1015 1020

Leu Ser Met Leu Phe Asn Met Gln Gly His Glu Asp Trp Val Leu Ser
 1025 1030 1035 1040

30 Leu His Cys Thr Ala Ser Tyr Leu Phe Ser Thr Ser Lys Asp Asn Val
 1045 1050 1055

35 Ile Lys Ile Trp Asp Leu Ser Asn Phe Ser Cys Ile Asp Thr Leu Lys
 1060 1065 1070

Gly His Trp Asn Ser Val Ser Ser Cys Val Val Lys Asp Arg Tyr Leu

1075

1080

1085

Tyr Ser Gly Ser Glu Asp Asn Ser Ile Lys Val Trp Asp Leu Asp Thr
 1090 1095 1100

5

Leu Glu Cys Val Tyr Thr Ile Pro Lys Ser His Ser Leu Gly Val Lys
 1105 1110 1115 1120

10

Cys Leu Met Val Phe Asn Asn Gln Ile Ile Ser Ala Ala Phe Asp Gly
 1125 1130 1135

Ser Ile Lys Val Trp Glu Trp Gln Ser Lys
 1140 1145

15 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

25

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Dictyostelium discoideum

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATAAGAAGAT AGAAGATGAT ATTTAAAGTT TGGTTTTTCAT ATGAAGATGA GGAAGTGGAA

60

35

CTATCAGAAT TAACAAATGA TACAACAGTG TCAGCAATTA GAAAGATCTT ACATGAAGGT

120

	AAAATATTTA GATTTCCATA TGGTACATCT CAAACAGACT TGCAAATTGG AAAGATGTTA	180
	CCATCTGGTA GTGGTGGAGG TGCAACTGCA GACAGCAAAT TTGAGAAGTT TAAAGCACGT	240
5	AATACATTAG CAGATATTCA ATATAAAGTT GGTGATACAT TATATGTTAG AGTTAAAAAA	300
	AGTAAACCAA CAAATGATTC ATTATTACCA ACATTAAATA TAGCATTTTT AGATGGATCA	360
	GAACGTGCAA TTAAATGGGA ATATGACCCA TATACTACAA CTGCTCAATG GACCTGTACA	420
10	GCAACATTAG TCAAAGTTGA ACCAGTACCA TTTGCTGAAG GTGCATTTAG GAAAGCTTAT	480
	CATACATTGG ATTTAAGTAA ATCTGGTGCA AGTGGAAGAT ATGTATCAAA GATTGGTAAA	540
15	AAACCAACAC CAAGACCATC ATATTTTGAA GATGTAAAGA TGCAAATGAT AGCAAAGAAA	600
	TGGGCAGATA AATATAATTC ATTTAAACCT CAAAAAAGA TTGAATTTTT ACAATCATGC	660
	GTTTTAGAGT TTGTAGATAG AACATCATCA GATTTAATTT GTGGAGCAGA ACCATATGTA	720
20	GAAGGACAAT ATAGAAAGTA TAATAATAAT AGTGGATTCG TTAGTAATGA TGAAAGAAAT	780
	ACACCACAAT CATTCTCTCA TTTCACATAT GAACATTCAA ATCATCAATT ATTGATTATA	840
25	GATATTCAAG GTGTTGGTGA TCACTATACA GACCCACAAA TTCATACCTA TGATGGTGTT	900
	GGTTTTGGTA TTGGTAATTT GGGTCAAAAA GGTTTTGAAA AGTTTTTTAGA TACTCATAAA	960
	TGTAATGCAA TTTGCCAATA TTAAATTTA CAATCAATTA ATCCAAAATC TGAAAAAAGT	1020
30	GATTGTGGTA CTGTACCAAG ACCAGATTTA ATTTTCCCTG ATACATCTGA AAGAGATAAT	1080
	AATAATAATA ATAATAATAA TAATAATAAT AATAATAATA ATAATAATAA TAATAGTAAT	1140
35	AATAATAATA ATAACAATAG TAGTATTTCA AAATCATTAG TTGAAATTC AAGTGGTAGT	1200
	AAAGAAAGAA ATGATAGAGA TTCGCCAAGT AGACAATTAT TTGTTTCAAA TGATGGTAAT	1260

ACATTAAATA CAAATAAAGA GAGATCAAAA TCAAAATCAA TAGATTTAGA AAAACCAGAA 1320
 ATTTTAATAA ATAATAAGAA AAAAGAGAGT ATAAATTTGG AAACGATAAA ATTAATTGAA 1380
 5 ACTATTAAAG GATATCATGT TACAAGTCAT TTATGTATTT GTGATAATTT ATTATTTACA 1440
 GGATGTTT CAG ATAATTCAAT TAGAGTGTAT GATTATAAGA GTCAAAATAT GGAATGTGTT 1500
 CAAACCTTGA AAGGTCATGA AGGTCCAGTT GAATCAATTT GTTATAATGA TCAATATTTG 1560
 10 TTTAGTGGTT CATCAGATCA TTCAATTAAA GTTTGGGATT TAAAGAAATT AAGATGTATT 1620
 TTTACTTTGG AGGGTCATGA TAAACCTGTC CATACGGTTC TATTGAATGA TAAATATTTG 1680
 15 TTTAGTGGTT CCTCTGACAA AACTATCAAA GTTTGGGATT TGAAAACTTT GGAATGTAAA 1740
 TATACCCTTG AAAGTCATGC CAGAGCCGTC AAAACACTTT GTATATCTGG TCAATATTTA 1800
 TTTAGTGGTT CAAATGATAA AACTATCAAG GTTTGGGATT TGAAAACTTT TCGTTGTAAC 1860
 20 TACTCTTAA AAGGTCATAC TAAATGGGTC ACCACTATCT GTATATTAGG TACCAATCTC 1920
 TACAGTGGCT CCTATGATAA AACTATAAGA GTTTGGAATT TAAAGAGTTT AGAATGTTCC 1980
 25 GCTACTTTAA GAGGCCATGA TAGATGSGTT GAACATATGG TAATTTGTGA TAAATTATTA 2040
 TTTACTGCTA GTGACGATAA TACAATTAAA ATTTGGGATT TAGAAACATT AAGATGTAAT 2100
 ACAACTTTGG AAGGACATAA TGCAACCGTT CAATGTTTAG CAGTTTGGGA AGATAAAAAA 2160
 30 TGTGTTATTA GTTGTAGTCA TGATCAAAGT ATTAGAGTTT GGGGTTGGAA TTAATTTAAA 2220
 ATAAAAA AAAACAT 2237

35 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Dictyostelium discoideum

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ile Phe Lys Val Trp Phe Ser Tyr Glu Asp Glu Glu Val Glu Leu
1 5 10 15

20

Ser Glu Leu Thr Asn Asp Thr Thr Val Ser Ala Ile Arg Lys Ile Leu
20 25 30

His Glu Gly Lys Ile Phe Arg Phe Pro Tyr Gly Thr Ser Gln Thr Asp
35 40 45

25

Leu Gln Ile Gly Lys Met Leu Pro Ser Gly Ser Gly Gly Ala Thr
50 55 60

30

Ala Asp Ser Lys Phe Glu Lys Phe Lys Ala Arg Asn Thr Leu Ala Asp
65 70 75 80

Ile Gln Tyr Lys Val Gly Asp Thr Leu Tyr Val Arg Val Lys Lys Ser
85 90 95

35

Lys Pro Thr Asn Asp Ser Leu Leu Pro Thr Leu Asn Ile Ala Phe Leu
100 105 110

	Asp	Gly	Ser	Glu	Arg	Ala	Ile	Lys	Trp	Glu	Tyr	Asp	Pro	Tyr	Thr	Thr	
	115				120				125								
5	Thr	Ala	Gln	Trp	Thr	Cys	Thr	Ala	Thr	Leu	Val	Lys	Val	Glu	Pro	Val	
	130				135				140								
	Pro	Phe	Ala	Glu	Gly	Ala	Phe	Arg	Lys	Ala	Tyr	His	Thr	Leu	Asp	Leu	
	145				150				155				160				
10	Ser	Lys	Ser	Gly	Ala	Ser	Gly	Arg	Tyr	Val	Ser	Lys	Ile	Gly	Lys	Lys	
					165				170				175				
	Pro	Thr	Pro	Arg	Pro	Ser	Tyr	Phe	Glu	Asp	Val	Lys	Met	Gln	Met	Ile	
					180				185				190				
15	Ala	Lys	Lys	Trp	Ala	Asp	Lys	Tyr	Asn	Ser	Phe	Lys	Pro	Pro	Lys	Lys	
	195				200				205								
	Ile	Glu	Phe	Leu	Gln	Ser	Cys	Val	Leu	Glu	Phe	Val	Asp	Arg	Thr	Ser	
20	210				215				220								
	Ser	Asp	Leu	Ile	Cys	Gly	Ala	Glu	Pro	Tyr	Val	Glu	Gly	Gln	Tyr	Arg	
	225				230				235				240				
25	Lys	Tyr	Asn	Asn	Asn	Ser	Gly	Phe	Val	Ser	Asn	Asp	Glu	Arg	Asn	Thr	
	245				250				255								
	Pro	Gln	Ser	Phe	Ser	His	Phe	Thr	Tyr	Glu	His	Ser	Asn	His	Gln	Leu	
	260				265				270								
30	Leu	Ile	Ile	Asp	Ile	Gln	Gly	Val	Gly	Asp	His	Tyr	Thr	Asp	Pro	Gln	
	275				280				285								
	Ile	His	Thr	Tyr	Asp	Gly	Val	Gly	Phe	Gly	Ile	Gly	Asn	Leu	Gly	Gln	
35	290				295				300								
	Lys	Gly	Phe	Glu	Lys	Phe	Leu	Asp	Thr	His	Lys	Cys	Asn	Ala	Ile	Cys	

305 310 315 320
 Gln Tyr Leu Asn Leu Gln Ser Ile Asn Pro Lys Ser Glu Lys Ser Asp
 325 330 335
 5 Cys Gly Thr Val Pro Arg Pro Asp Leu Ile Phe Pro Asp Thr Ser Glu
 340 345 350
 Arg Asp Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
 10 355 360 365
 Asn Asn Asn Asn Asn Ser Asn Asn Asn Asn Asn Asn Asn Ser Ser Ile
 370 375 380
 15 Ser Lys Ser Leu Val Glu Ile Ser Ser Gly Ser Lys Glu Arg Asn Asp
 385 390 395 400
 Arg Asp Ser Pro Ser Arg Gln Leu Phe Val Ser Asn Asp Gly Asn Thr
 20 405 410 415
 Leu Asn Thr Asn Lys Glu Arg Ser Lys Ser Lys Ser Ile Asp Leu Glu
 420 425 430
 Lys Pro Glu Ile Leu Ile Asn Asn Lys Lys Lys Glu Ser Ile Asn Leu
 25 435 440 445
 Glu Thr Ile Lys Leu Ile Glu Thr Ile Lys Gly Tyr His Val Thr Ser
 450 455 460
 30 His Leu Cys Ile Cys Asp Asn Leu Leu Phe Thr Gly Cys Ser Asp Asn
 465 470 475 480
 Ser Ile Arg Val Tyr Asp Tyr Lys Ser Gln Asn Met Glu Cys Val Gln
 485 490 495
 35 Thr Leu Lys Gly His Glu Gly Pro Val Glu Ser Ile Cys Tyr Asn Asp
 500 505 510

Gln Tyr Leu Phe Ser Gly Ser Ser Asp His Ser Ile Lys Val Trp Asp
 515 520 525

5 Leu Lys Lys Leu Arg Cys Ile Phe Thr Leu Glu Gly His Asp Lys Pro
 530 535 540

Val His Thr Val Leu Leu Asn Asp Lys Tyr Leu Phe Ser Gly Ser Ser
 545 550 555 560

10 Asp Lys Thr Ile Lys Val Trp Asp Leu Lys Thr Leu Glu Cys Lys Tyr
 565 570 575

Thr Leu Glu Ser His Ala Arg Ala Val Lys Thr Leu Cys Ile Ser Gly
 580 585 590

15 Gln Tyr Leu Phe Ser Gly Ser Asn Asp Lys Thr Ile Lys Val Trp Asp
 595 600 605

20 Leu Lys Thr Phe Arg Cys Asn Tyr Thr Leu Lys Gly His Thr Lys Trp
 610 615 620

Val Thr Thr Ile Cys Ile Leu Gly Thr Asn Leu Tyr Ser Gly Ser Tyr
 625 630 635 640

25 Asp Lys Thr Ile Arg Val-Trp Asn Leu Lys Ser Leu Glu Cys Ser Ala
 645 650 655

Thr Leu Arg Gly His Asp Arg Trp Val Glu His Met Val Ile Cys Asp
 660 665 670

30 Lys Leu Leu Phe Thr Ala Ser Asp Asp Asn Thr Ile Lys Ile Trp Asp
 675 680 685

35 Leu Glu Thr Leu Arg Cys Asn Thr Thr Leu Glu Gly His Asn Ala Thr
 690 695 700

Val Gln Cys Leu Ala Val Trp Glu Asp Lys Lys Cys Val Ile Ser Cys

705

710

715

720

Ser His Asp Gln Ser Ile Arg Val Trp Gly Trp Asn
725 730

5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 2307 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

15

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: C. elegans

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

25 ATGACGATCG ACACAACAAA TGAGAGCGAC AATAGTCCAA CTAAC TCACC AGGATTGGAG 60
GCCTCGGCTC GGACATTCTC GCTCAATGCG TCAAAAATGG TTCGGATAAC CGACGACTAC 120
GCAGATGAAG TGTTCATTGA ACAGAATGAT GTCGTTATCG AGAAGCCTCG TATGGATCCT 180
30 CTCCACGTTA GAAAACTTAT GGAGACATGG CGCAAGGCTG CTCGCCGAGC AAGAACAAAC 240
TATATAGATC CATGGGATGA GTTCAACATC CACGAGTATC CAGTACAACG AGCTAAACGA 300
35 TATAGGTATT CTGCAATCAG AAAGCAATGG ACAGAGGATA TAGTCGATGT GAGACTTCAT 360
CCGGACAGTT TTGCACGTGG AGCCATGCCA GAATGCTACC GACTCAAAAA GTGCTCCAAG 420

	CACGGAACAA GTCAAGATTG GAGCAGCAAC TATGTCGCAA AAAGATACAT TTGTCAAGTC	480
	GATCGTAGAG TTCTTTTCGA TGATGTCAGA CTTCAGATGG ATGCCAAATT ATGGGCTGAA	540
5	GAATATAATC GGTATAATCC ACCGAAGAAA ATTGATATTG TTCAAATGTG TGTCATTGAG	600
	ATGATTGATG TAAAAGGTTC TCCACTCTAT CATTTGGAGC ATTTTCATCGA GGGAAAATAT	660
	ATAAAATACA ATTCAAACCTC AGGATTTGTA TCAAATGCAG CTCGTCTTAC ACCACAAGCA	720
10	TTTTCTCACT TCACCTTCGA ACGTTCTGGT CATCAAATGA TGGTTGTCGA TATTCAAGGA	780
	GTTGGTGATC TTTACACAGA TCCTCAGATT CATAAGTTG TGGGAAGTGA TTATGGAGAT	840
15	GGAAACCTCG GAACTCGTGG AATGGCTCTT TTCTTCCATT CACACAGATG TAACGATATT	900
	TGTGAGACAA TGGATCTATC AAATTTTCGAA CTTTCGCCAC CTGAAATCGA GGCTACCGAA	960
	GTTGCGATGG AAGTAGCTGC AAAGCAGAAA AAGTCATGCA TAGTTCCTCC AACTGTGTTC	1020
20	GAAGCAAGAA GAAATCGAAT TTCAAGTGAA TGTGTACATG TCGAGCATGG TATTTTCGATG	1080
	GATCAATTGA GAAAAAGGAA GACGTTGAAT CAATCGTCAA CCGATTTGTC AGCAAAGAGT	1140
25	CACAACGAAG ACTGTGTATG TCCTGAGTGT ATTCCAGTTG TTGAGCAACT CTGTGAGCCT	1200
	TGCTCCGAAG ATGAAGAGGA CGAAGAAGAA GACTATCCAA GAAGTGAAAA AAGTGGAAT	1260
	AGTCAGAAAA GTCGACGTAG TAGAATGAGC ATTTCAACGA GATCTTCTGG CGATGAATCA	1320
30	GCATCTCGTC CTAGAAAATG CGGATTTGTA GATTTAACT CACTTCGTCA GAGACATGAT	1380
	AGCTTCAGAA GTTCTGTTGG GACATATTCT ATGAATAGTT CTAGACAAAC CAGAGACACT	1440
35	GAAAAGGATG AATTCTGGAA GGTTCCTTCGA AAACAATCAG TTCCAGCAAA CATTCTATCA	1500
	CTTCAACTTC AACAAATGGC TGCTAACCTG GAAAATGATG AAGACGTACC ACAAGTCACC	1560

GGGCATCAGT TCTCTGTCCT CGGTCAGATT CATATTGATC TCTCACGATA TCATGAGCTC 1620

GGGCGGTTCG TAGAAGTTGA TTCAGAACAT AAGGAAATGC TTGAGGGAAG TGAAAATGAC 1680

5 GCTCGTGTAC CAATCAAATA CGACAAGCAG TCTGCAATTT TCCATTTGGA TATCGCTCGG 1740

AAGTGTGGAA TCCTTGAGGC TGTGCTAACA TCGGCTCATA TTGTTCTCGG ATTACCACAT 1800

GAATTGTTGA AAGAAGTCAC CGTTGATGAT CTGTTTCCTA ATGGGTTTGG AGAACAGGAA 1860

10 AATGGAATTC GAGCTGATAA AGGACAAAAA CCTTGTGACC TAGAAGAGTT CGGCTCCGAT 1920

CTGATGGAAA TTGCTGCAGA GATGGGTGAT AAGGGTGCAA TGCTGTACAT GGCACACGCT 1980

15 TATGAAACTG GTCAGCATCT CGGACCGAAT CGAAGAACGG ATTATAAGAA ATCGATTGAT 2040

TGGTATCAAC GCGTCGTTGG ATTCCAAGAA GAAGAAGAAC TTGACTCTGA TTGTGGAAAA 2100

ACGACATTCT CCTCATTTGC TCCACTGACT CGTCACGAGA TTCTAGCCAA AATGGCTGAA 2160

20 ATGTACAAAG AGGGAGGTTA TGGCCTGAAT CAAGACTTCG AACGAGCATA TGGTCTATTC 2220

AATGAAGCTG CTGAAGCAGC AATGGAAGCA ATGAATGGAA AGCTCGCAAA TAAATACTAT 2280

25 GAAAAAGCGG AAATGTGTGG AGAATGA 2307

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 768 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *C. elegans*

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Thr Ile Asp Thr Thr Asn Glu Ser Asp Asn Ser Pro Thr Asn Ser
 1 5 10 15
 Pro Gly Leu Glu Ala Ser Ala Arg Thr Phe Ser Leu Asn Ala Ser Lys
 20 25 30
 Met Val Arg Ile Thr Asp Asp Tyr Ala Asp Glu Val Phe Ile Glu Gln
 15 35 40 45
 Asn Asp Val Val Ile Glu Lys Pro Arg Met Asp Pro Leu His Val Arg
 50 55 60
 Lys Leu Met Glu Thr Trp Arg Lys Ala Ala Arg Arg Ala Arg Thr Asn
 20 65 70 75 80
 Tyr Ile Asp Pro Trp Asp Glu Phe Asn Ile His Glu Tyr Pro Val Gln
 85 90 95
 Arg Ala Lys Arg Tyr Arg Tyr Ser Ala Ile Arg Lys Gln Trp Thr Glu
 100 105 110
 Asp Ile Val Asp Val Arg Leu His Pro Asp Ser Phe Ala Arg Gly Ala
 30 115 120 125
 Met Arg Glu Cys Tyr Arg Leu Lys Lys Cys Ser Lys His Gly Thr Ser
 130 135 140
 Gln Asp Trp Ser Ser Asn Tyr Val Ala Lys Arg Tyr Ile Cys Gln Val
 35 145 150 155 160

	Asp Arg Arg Val Leu Phe Asp Asp Val Arg Leu Gln Met Asp Ala Lys	165	170	175
5	Leu Trp Ala Glu Glu Tyr Asn Arg Tyr Asn Pro Pro Lys Lys Ile Asp	180	185	190
	Ile Val Gln Met Cys Val Ile Glu Met Ile Asp Val Lys Gly Ser Pro	195	200	205
10	Leu Tyr His Leu Glu His Phe Ile Glu Gly Lys Tyr Ile Lys Tyr Asn	210	215	220
	Ser Asn Ser Gly Phe Val Ser Asn Ala Ala Arg Leu Thr Pro Gln Ala	225	230	235
15	Phe Ser His Phe Thr Phe Glu Arg Ser Gly His Gln Met Met Val Val	245	250	255
	Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp Pro Gln Ile His Thr	260	265	270
20	Val Val Gly Thr Asp Tyr Gly Asp Gly Asn Leu Gly Thr Arg Gly Met	275	280	285
	Ala Leu Phe Phe His Ser His Arg Cys Asn Asp Ile Cys Glu Thr Met	290	295	300
	Asp Leu Ser Asn Phe Glu Leu Ser Pro Pro Glu Ile Glu Ala Thr Glu	305	310	315
30	Val Ala Met Glu Val Ala Ala Lys Gln Lys Lys Ser Cys Ile Val Pro	325	330	335
	Pro Thr Val Phe Glu Ala Arg Arg Asn Arg Ile Ser Ser Glu Cys Val	340	345	350
35	His Val Glu His Gly Ile Ser Met Asp Gln Leu Arg Lys Arg Lys Thr			

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Glu Val Asp Ser Glu His Lys Glu Met Leu Glu Gly Ser Glu Asn Asp
545 550 555 560

Ala Arg Val Pro Ile Lys Tyr Asp Lys Gln Ser Ala Ile Phe His Leu
565 570 575

5 Asp Ile Ala Arg Lys Cys Gly Ile Leu Glu Ala Val Leu Thr Ser Ala
580 585 590

His Ile Val Leu Gly Leu Pro His Glu Leu Leu Lys Glu Val Thr Val
595 600 605

10 Asp Asp Leu Phe Pro Asn Gly Phe Gly Glu Gln Glu Asn Gly Ile Arg
610 615 620

Ala Asp Lys Gly Gln Lys Pro Cys Asp Leu Glu Glu Phe Gly Ser Asp
625 630 635 640

15 Leu Met Glu Ile Ala Ala Glu Met Gly Asp Lys Gly Ala Met Leu Tyr
645 650 655

20 Met Ala His Ala Tyr Glu Thr Gly Gln His Leu Gly Pro Asn Arg Arg
660 665 670

Thr Asp Tyr Lys Lys Ser Ile Asp Trp Tyr Gln Arg Val Val Gly Phe
675 680 685

25 Gln Glu Glu Glu Glu Leu Asp Ser Asp Cys Gly Lys Thr Thr Phe Ser
690 695 700

Ser Phe Ala Pro Leu Thr Arg His Glu Ile Leu Ala Lys Met Ala Glu
705 710 715 720

30 Met Tyr Lys Glu Gly Gly Tyr Gly Leu Asn Gln Asp Phe Glu Arg Ala
725 730 735

35 Tyr Gly Leu Phe Asn Glu Ala Ala Glu Ala Ala Met Glu Ala Met Asn
740 745 750

Gly Lys Leu Ala Asn Lys Tyr Tyr Glu Lys Ala Glu Met Cys Gly Glu

(2) INFORMATION FOR SEQ ID NO:11:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2283 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: C. elegans

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGACGATCG ACACAACAAA TGAGAGCGAC AATAGTCCAA CTAAC TCACC AGGATTGGAG 60

25 GCCTCGGCTC GGACATTCTC GCTCAATGCG TCAAAAATGG TTCGGATAAC CGACGACTAC 120

GCAGATGAAG TGTTTCATTGA ACAGAATGAT GTCGTTATCG AGAAGCCTCG TATGGATCCT 180

30 CTCCACGTTA GAAAACTTAT GGAGACATGG CGCAAGGCTG CTCGCCGAGC AAGAACAAAC 240

TATATAGATC CATGGGATGA GTTCAACATC CACGAGTATC CAGTACAACG AGCTAAACGA 300

TATAGGTATT CTGCAATCAG AAAGCAATGG ACAGAGGATA TAGTCGATGT GAGACTTCAT 360

35 CCGGACAGTT TTGCACGTGG AGCCATGCGA GAATGCTACC GACTCAAAAA GTGCTCCAAG 420

CACGGAACAA GTCAAGATTG GAGCAGCAAC TATGTCGCAA AAAGATACAT TTGTCAAGTC 480

GATCGTAGAG TTCTTTTCGA TGATGTCAGA CTTCAGATGG ATGCCAAATT ATGGGCTGAA 540
 GAATATAATC GGTATAATCC ACCGAAGAAA ATTGATATTG TTCAAATGTG TGTCATTGAG 600
 5 ATGATTGATG TAAAAGGTTC TCCACTCTAT CATTGGAGC ATTCATCGA GGGAAAATAT 660
 ATAAAATACA ATTCAAATC AGGATTTGTA TCAAATGCAG CTCGTCTTAC ACCACAAGCA 720
 TTTTCTCACT TCACCTTCGA ACGTTCTGGT CATCAAATGA TGGTTGTCGA TATTCAAGGA 780
 10 GTTGGTGATC TTTACACAGA TCCTCAGATT CATAAGTTG TGGGAACTGA TTATGGAGAT 840
 GGAAACCTCG GAACTCGTGG AATGGCTCTT TTCTTCCATT CACACAGATG TAACGATATT 900
 15 TGTGAGACAA TGGATCTATC AAATTTTCGAA CTTTCGCCAC CTGAAATCGA GGCTACCGAA 960
 GTTGCGATGG AAGTAGCTGC AAAGCAGAAA AAGTCATGCA TAGTTCCTCC AACTGTGTTC 1020
 GAAGCAAGAA GAAATCGAAT TTCAAGTGAA TGTGTACATG TCGAGCATGG TATTTTCGATG 1080
 20 GATCAATTGA GAAAAAGGAA GACGTTGAAT CAATCGTCAA CCGATTTGTC AGCAAAGAGT 1140
 CACAACGAAG ACTGTGTATG TCCTGAGTGT ATTCCAGTTG TTGAGCAACT CTGTGAGCCT 1200
 25 TGCTCCGAAG ATGAAGAGGA CGAAGAAGAA GACTATCCAA GAAGTGAAAA AAGTGGAAT 1260
 AGTCAGAAAA GTCGACGTAG TAGAATGAGC ATTTCAACGA GATCTTCTGG CGATGAATCA 1320
 GCATCTCGTC CTAGAAAATG CGGATTTGTA GATTTAAACT CACTTCGTCA GAGACATGAT 1380
 30 AGCTTCAGAA GTTCTGTTGG GACATATTCT ATGAATAGTT CTAGACAAAC CAGAGACACT 1440
 GAAAAGGATG AATTCTGGAA GGTTCCTCGA AAACAATCAG TTCCAGCAAA CATTCTATCA 1500
 35 CTTCAACTTC AACAAATGGC TGCTAACCTG GAAAATGATG AAGACGTACC ACAAGTCACC 1560
 GGGCATCAGT TCTCTGTCCT CGGTCAGATT CATATTGATC TCTCAGATA TCATGAGCTC 1620

GGGCGGTTTCG TAGAAGTTGA TTCAGAACAT AAGGAAATGC TTGAGGGAAG TGAAAATGAC 1680
GCTCGTGTAC CAATCAAATA CGACAAGCAG TCTGCAATTT TCCATTTGGA TATCGCTCGG 1740
5 AAGTGTGGAA TCCTTGAGGC TGTGCTAACA TCGGCTCATA TTGTTCTCGG ATTACCACAT 1800
GAATTGTTGA AAGAAGTCAC CGTTGATGAT CTGTTTCCTA ATGGGTTTGG AGAACAGGAA 1860
AATGGAATTC GAGACCTAGA AGAGTTCGGC TCCGATCTGA TGGAAATTGC TGCAGAGATG 1920
10 GGTGATAAGG GTGCAATGCT GTACATGGCA CACGCTTATG AAATGGTCA GCATCTCGGA 1980
CCGAATCGAA GAACGGATTA TAAGAAATCG ATTGATTGGT ATCAACGCGT CGTTGGATTC 2040
15 CAAGAAGAAG AAGAACTGA CTCTGATTGT GGAAAAACGA CATTCTCCTC ATTTGCTCCA 2100
CTGACTCGTC ACGAGATTCT AGCCAAAATG GCTGAAATGT ACAAAGAGGG AGGTTATGGC 2160
CTGAATCAAG ACTTCGAACG AGCATATGGT CTATTCAATG AAGCTGCTGA AGCAGCAATG 2220
20 GAAGCAATGA ATGGAAAGCT CGCAAATAAA TACTATGAAA AAGCGGAAAT GTGTGGAGAA 2280
TGA 2283

25 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 760 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: C. elegans

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Thr Ile Asp Thr Thr Asn Glu Ser Asp Asn Ser Pro Thr Asn Ser
 1 5 10 15

10 Pro Gly Leu Glu Ala Ser Ala Arg Thr Phe Ser Leu Asn Ala Ser Lys
 20 25 30

Met Val Arg Ile Thr Asp Asp Tyr Ala Asp Glu Val Phe Ile Glu Gln
 35 40 45

15 Asn Asp Val Val Ile Glu Lys Pro Arg Met Asp Pro Leu His Val Arg
 50 55 60

Lys Leu Met Glu Thr Trp Arg Lys Ala Ala Arg Arg Ala Arg Thr Asn
 20 65 70 75 80

Tyr Ile Asp Pro Trp Asp Glu Phe Asn Ile His Glu Tyr Pro Val Gln
 85 90 95

25 Arg Ala Lys Arg Tyr Arg Tyr Ser Ala Ile Arg Lys Gln Trp Thr Glu
 100 105 110

Asp Ile Val Asp Val Arg Leu His Pro Asp Ser Phe Ala Arg Gly Ala
 115 120 125

30 Met Arg Glu Cys Tyr Arg Leu Lys Lys Cys Ser Lys His Gly Thr Ser
 130 135 140

Gln Asp Trp Ser Ser Asn Tyr Val Ala Lys Arg Tyr Ile Cys Gln Val
 35 145 150 155 160

Asp Arg Arg Val Leu Phe Asp Asp Val Arg Leu Gln Met Asp Ala Lys

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Leu Trp Ala Glu Glu Tyr Asn Arg Tyr Asn Pro Pro Lys Lys Ile Asp
 180 185 190

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Ile Val Gln Met Cys Val Ile Glu Met Ile Asp Val Lys Gly Ser Pro
 195 200 205

10

Leu Tyr His Leu Glu His Phe Ile Glu Gly Lys Tyr Ile Lys Tyr Asn
 210 215 220

Ser Asn Ser Gly Phe Val Ser Asn Ala Ala Arg Leu Thr Pro Gln Ala
 225 230 235 240

15

Phe Ser His Phe Thr Phe Glu Arg Ser Gly His Gln Met Met Val Val
 245 250 255

20

Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp Pro Gln Ile His Thr
 260 265 270

Val Val Gly Thr Asp Tyr Gly Asp Gly Asn Leu Gly Thr Arg Gly Met
 275 280 285

25

Ala Leu Phe Phe His Ser His Arg Cys Asn Asp Ile Cys Glu Thr Met
 290 295 300

Asp Leu Ser Asn Phe Glu Leu Ser Pro Pro Glu Ile Glu Ala Thr Glu
 305 310 315 320

30

Val Ala Met Glu Val Ala Ala Lys Gln Lys Lys Ser Cys Ile Val Pro
 325 330 335

Pro Thr Val Phe Glu Ala Arg Arg Asn Arg Ile Ser Ser Glu Cys Val
 340 345 350

35

His Val Glu His Gly Ile Ser Met Asp Gln Leu Arg Lys Arg Lys Thr
 355 360 365

5 Cys Val Cys Pro Glu Cys Ile Pro Val Val Glu Gln Leu Cys Glu Pro
385 390 395 400

10 Lys Ser Gly Asn Ser Gln Lys Ser Arg Arg Ser Arg Met Ser Ile Ser
 420 425 430

15 Phe Val Asp Leu Asn Ser Leu Arg Gln Arg His Asp Ser Phe Arg Ser
450 455 460

20 465 470 475 480

Glu Lys Asp Glu Phe Trp Lys Val Leu Arg Lys Gln Ser Val Pro Ala

485 490 495

25 Asn Ile Leu Ser Leu Gln-Leu Gln Gln Met Ala Ala Asn Leu Glu Asn
500 505 510

30

Gln Ile His Ile Asp Leu Ser Arg Tyr His Glu Leu Gly Arg Phe Val

530 535 540

Glu Val Asp Ser Glu His Lys Glu Met Leu Glu Gly Ser Glu Asn Asp
35 545 550 555 560

Ala Arg Val Pro Ile Lys Tyr Asp Lys Gln Ser Ala Ile Phe His Leu

565

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Asp Ile Ala Arg Lys Cys Gly Ile Leu Glu Ala Val Leu Thr Ser Ala
 580 585 590

5

His Ile Val Leu Gly Leu Pro His Glu Leu Leu Lys Glu Val Thr Val
 595 600 605

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Asp Asp Leu Phe Pro Asn Gly Phe Gly Glu Gln Glu Asn Gly Ile Arg
 610 615 620

Asp Leu Glu Glu Phe Gly Ser Asp Leu Met Glu Ile Ala Ala Glu Met
 625 630 635 640

15

Gly Asp Lys Gly Ala Met Leu Tyr Met Ala His Ala Tyr Glu Thr Gly
 645 650 655

Gln His Leu Gly Pro Asn Arg Arg Thr Asp Tyr Lys Lys Ser Ile Asp
 660 665 670

20

Trp Tyr Gln Arg Val Val Gly Phe Gln Glu Glu Glu Glu Leu Asp Ser
 675 680 685

25

Asp Cys Gly Lys Thr Thr Phe Ser Ser Phe Ala Pro Leu Thr Arg His
 690 695 700

Glu Ile Leu Ala Lys Met Ala Glu Met Tyr Lys Glu Gly Gly Tyr Gly
 705 710 715 720

30

Leu Asn Gln Asp Phe Glu Arg Ala Tyr Gly Leu Phe Asn Glu Ala Ala
 725 730 735

Glu Ala Ala Met Glu Ala Met Asn Gly Lys Leu Ala Asn Lys Tyr Tyr
 740 745 750

35

Glu Lys Ala Glu Met Cys Gly Glu
 755 760

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 628 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: Dictyostelium discoideum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

20 GTATTGTATG TGTTC AATT GAGAAGACTC CATTTCGAAA GGGTAGTTGT AGAACAGCAC 60
ATAAATTAAA GGATTGGAGT CAACCAGATC AAGGATTAGT TGGTAAATTT TCAACCAATA 120
AAAAGACGAC AAGAGATTCA TACTTTACAG ATGTATTGAT GCAAACATTT TGTGCTAAAT 180
25 GGGCAGAGAA ATTCAATGAA GCGAAACCAC CAAAACCAAT TACATTCTTA CCATCATACG 240
TTTACGAATT GATTGATCAT CCACCACCTT ATCCAGTTTG TGGTGGTGAA CCATTCATTG 300
30 AGGGAGATTA CAAGAAACAT AACAACAACA GTGGTTACGT TAGTAGTGAT GCTAGAAATA 360
CACCACAATC ATTCTCTCAT TTCTCATACG AACTCTCCAA TCATGAATTG TTGATCGTTG 420
ATATCCAAGG TGTCAACGAT TTCTTACTG ATCCTCAAAT TCATACGAAA TCAGGCGAGG 480
35 GCTTTGGCGA GGGTAATTTG GGCGAGACGG GTTCCACAA ATTCCTTCAA ACACACAAGT 540

GTAATCCAGT TTGTGACTTT TTAAAGTTGA AACCAATCAA TCAATCAAAG AAAGCCCTCC

600

TAAGAGGTAC ATTACCCGTC GTACAATT

628

5 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Dictyostelium discoideum

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

25 Ile Val Cys Val Ser Ile Glu Lys Thr Pro Phe Ala Lys Gly Ser Cys
1 5 10 15

Arg Thr Ala His Lys Leu Lys Asp Trp Ser Gln Pro Asp Gln Gly Leu
20 25 30

30 Val Gly Lys Phe Ser Thr Asn Lys Lys Thr Thr Arg Asp Ser Tyr Phe
35 40 45

Thr Asp Val Leu Met Gln Thr Phe Cys Ala Lys Trp Ala Glu Lys Phe
50 55 60

35

Asn Glu Ala Lys Pro Pro Lys Pro Ile Thr Phe Leu Pro Ser Tyr Val
65 70 75 80

Tyr Glu Leu Ile Asp His Pro Pro Pro Tyr Pro Val Cys Gly Gly Glu
 85 90 95

5 Pro Phe Ile Glu Gly Asp Tyr Lys Lys His Asn Asn Asn Ser Gly Tyr
 100 105 110

Val Ser Ser Asp Ala Arg Asn Thr Pro Gln Ser Phe Ser His Phe Ser
 115 120 125

10 Tyr Glu Leu Ser Asn His Glu Leu Leu Ile Val Asp Ile Gln Gly Val
 130 135 140

Asn Asp Phe Tyr Thr Asp Pro Gln Ile His Thr Lys Ser Gly Glu Gly
 145 150 155 160

15 Phe Gly Glu Gly Asn Leu Gly Glu Thr Gly Phe His Lys Phe Leu Gln
 165 170 175

Thr His Lys Cys Asn Pro Val Cys Asp Phe Leu Lys Leu Lys Pro Ile
 20 180 185 190

Asn Gln Ser Lys Lys Ala Leu Leu Arg Gly Thr Leu Pro Val Val Gln
 195 200 205

25 Leu

(2) INFORMATION FOR SEQ ID NO:15:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

10 Gly Glu Trp Leu Asp Asp Glu Val Leu Ile Lys Met Ala Ser Gln Pro
1 5 10 15

Phe Gly Arg Gly Ala Met Arg Glu Cys Phe Arg Thr Lys Lys Leu Ser
20 25 30

15 Asn Phe Leu His Ala Gln Gln Trp Lys Gly Ala Ser Asn Tyr Val Ala
35 40 45

Lys Arg Tyr Ile Glu Pro Val Asp Arg Asp Val Tyr Phe Glu Asp Val
20 50 55 60

Arg Leu Gln Met Glu Ala Lys Leu Trp Gly Glu Glu Tyr Asn Arg His
65 70 75 80

25 Lys Pro Pro Lys Gln Val Asp Ile Met Gln Met Cys Ile Ile Glu Leu
85 90 95

Lys Asp Arg Pro Gly Lys Pro Leu Phe His Leu Glu His Tyr Ile Glu
100 105 110

30 Gly Lys Tyr Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Arg Asp Asp
115 120 125

Asn Ile Arg Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg
35 130 135 140

Ser Gly His Gln Leu Ile Val Val Asp Ile Gln Gly Val Gly Asp Leu

145 150 155 160
 Tyr Thr Asp Pro Gln Ile His Thr Glu Thr Gly Thr Asp Phe Gly Asp
 165 170 175
 5 Gly Asn Leu Gly Val Arg Gly Met Ala Leu Phe Phe Tyr Ser His Ala
 180 185 190
 Cys Asn Arg Ile Cys Glu Ser Met Gly Leu Ala Pro Phe Asp Leu Ser
 10 195 200 205
 Pro Arg Glu Arg Asp Ala Val Asn Gln Asn Thr Lys Leu Leu Gln Ser
 210 215 220
 15 Ala Lys Thr Ile Leu Arg Gly Thr Glu Glu Lys Cys Gly Ser
 225 230 235

(2) INFORMATION FOR SEQ ID NO:16:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 258 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- 25 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

- 30 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: D. discoideum

- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn Lys Trp Ile Arg Leu Ser Met Lys Leu Lys Val Glu Arg Lys Pro

	1	5	10	15
	Phe	Ala	Glu	Gly
		Ala	Leu	Arg
			Glu	Ala
			Tyr	His
			Thr	Val
			Ser	Leu
			Gly	
	20		25	30
5	Val	Gly	Thr	Asp
		Glu	Asn	Tyr
		Pro	Leu	Gly
			Thr	Thr
			Thr	Lys
			Leu	Phe
	35		40	45
	Pro	Pro	Ile	Glu
		Met	Ile	Ser
		Pro	Ile	Ser
			Lys	Asn
			Asn	Glu
			Ala	Met
10	50		55	60
	Thr	Gln	Leu	Lys
		Asn	Gly	Thr
		Lys	Phe	Val
		Leu	Lys	Leu
		Tyr	Lys	Lys
	65		70	75
				80
	Glu	Ala	Glu	Gln
		Gln	Ala	Ser
		Arg	Glu	Leu
		Tyr	Phe	Glu
		Asp	Val	Lys
15		85	90	95
	Met	Gln	Met	Val
		Cys	Arg	Asp
		Trp	Gly	Asn
		Lys	Phe	Asn
		Gln	Lys	Lys
	100		105	110
20	Pro	Pro	Lys	Lys
		Ile	Glu	Phe
		Leu	Met	Ser
		Trp	Val	Val
		Glu	Leu	Ile
	115		120	125
	Asp	Arg	Ser	Pro
		Ser	Ser	Asn
		Gly	Gln	Pro
		Ile	Leu	Cys
		Ser	Ile	Glu
25	130		135	140
	Pro	Leu	Leu	Val
		Gly	Glu	Phe
		Lys	Lys	Asn
		Asn	Ser	Asn
		Tyr	Gly	Ala
	145		150	155
				160
	Val	Leu	Thr	Asn
		Arg	Ser	Thr
		Pro	Gln	Ala
		Phe	Ser	His
		Phe	Thr	Tyr
30		165	170	175
	Glu	Leu	Ser	Asn
		Lys	Gln	Met
		Ile	Val	Val
		Asp	Ile	Gln
		Gly	Val	Asp
	180		185	190
35	Asp	Leu	Tyr	Thr
		Asp	Pro	Gln
		Ile	His	Thr
		Pro	Asp	Gly
		Lys	Gly	Phe
	195		200	205

Gly Leu Gly Asn Leu Gly Lys Ala Gly Ile Asn Lys Phe Ile Thr Thr
 210 215 220

5 His Lys Cys Asn Ala Val Cys Ala Leu Leu Asp Leu Asp Val Lys Leu
 225 230 235 240

Gly Gly Val Leu Ser Gly Asn Asn Lys Lys Gln Leu Gln Gln Gly Thr
 245 250 255

10 Met Val

(2) INFORMATION FOR SEQ ID NO:17:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: D. discoideum

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ala Gln Trp Thr Cys Thr Ala Thr Leu Val Lys Val Glu Pro Val Pro
 1 5 10 15

35 Phe Ala Glu Gly Ala Phe Arg Lys Ala Tyr His Thr Leu Asp Leu Ser
 20 25 30

	Lys	Ser	Gly	Ala	Ser	Gly	Arg	Tyr	Val	Ser	Lys	Ile	Gly	Lys	Lys	Pro	
			35					40					45				
5	Thr	Pro	Arg	Pro	Ser	Tyr	Phe	Glu	Asp	Val	Lys	Met	Gln	Met	Ile	Ala	
		50					55					60					
	Lys	Lys	Trp	Ala	Asp	Lys	Tyr	Asn	Ser	Phe	Lys	Pro	Pro	Lys	Lys	Ile	
	65					70					75				80		
10	Glu	Phe	Leu	Gln	Ser	Cys	Val	Leu	Glu	Phe	Val	Asp	Arg	Thr	Ser	Ser	
					85						90				95		
	Asp	Leu	Ile	Cys	Gly	Ala	Glu	Pro	Tyr	Val	Glu	Gly	Gln	Tyr	Arg	Lys	
				100					105					110			
15	Tyr	Asn	Asn	Asn	Ser	Gly	Phe	Val	Ser	Asn	Asp	Glu	Arg	Asn	Thr	Pro	
				115				120					125				
	Gln	Ser	Phe	Ser	His	Phe	Thr	Tyr	Glu	His	Ser	Asn	His	Gln	Leu	Leu	
20		130					135					140					
	Ile	Ile	Asp	Ile	Gln	Gly	Val	Gly	Asp	His	Tyr	Thr	Asp	Pro	Gln	Ile	
	145				150					155					160		
25	His	Thr	Tyr	Asp	Gly	Val	Gly	Phe	Gly	Ile	Gly	Asn	Leu	Gly	Gln	Lys	
					165					170					175		
	Gly	Phe	Glu	Lys	Phe	Leu	Asp	Thr	His	Lys	Cys	Asn	Ala	Ile	Cys	Gln	
				180					185					190			
30	Tyr	Leu	Asn	Leu	Gln	Ser	Ile	Asn	Pro	Lys	Ser	Glu	Lys	Ser	Asp	Cys	
			195					200					205				
	Gly	Thr	Val	Pro													
35																	210

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: C. elegans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys Gln Trp Thr Glu Asp Ile Val Asp Val Arg Leu His Pro Asp Ser
 1 5 10 15

Phe Ala Arg Gly Ala Met Arg Glu Cys Tyr Arg Leu Lys Lys Cys Ser
 20 25 30

Lys His Gly Thr Ser Gln Asp Trp Ser Ser Asn Tyr Val Ala Lys Arg
 25 35 40 45

Tyr Ile Cys Gln Val Asp Arg Arg Val Leu Phe Asp Asp Val Arg Leu
 50 55 60

Gln Met Asp Ala Lys Leu Trp Ala Glu Glu Tyr Asn Arg Tyr Asn Pro
 65 70 75 80

Pro Lys Lys Ile Asp Ile Val Gln Met Cys Val Ile Glu Met Ile Asp
 85 90 95

Val Lys Gly Ser Pro Leu Tyr His Leu Glu His Phe Ile Glu Gly Lys
 100 105 110

Tyr Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Ser Asn Ala Ala Arg
 115 120 125

5 Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His
 130 135 140

Gln Met Met Val Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp
 145 150 155 160

10 Pro Gln Ile His Thr Val Val Gly Thr Asp Tyr Gly Asp Gly Asn Leu
 165 170 175

Gly Thr Arg Gly Met Ala Leu Phe Phe His Ser His Arg Cys Asn Asp
 180 185 190

15 Ile Cys Glu Thr Met Asp Leu Ser Asn Phe Glu Leu Ser Pro Pro Glu
 195 200 205

20 Ile Glu Ala Thr Glu Val Ala Met Glu Val Ala Ala Lys Gln Lys Lys
 210 215 220

Ser Cys Ile Val Pro Pro Thr Val Phe
 225 230

25 (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35 (A) DESCRIPTION: /desc = "Oligonucleotide Primer D"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5 GGATTGGAC TGGACAAGAA CCCC

25

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

25 Arg Lys Lys Phe Gly Glu Ser Glu Lys Thr Lys Thr Lys Glu Phe Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:21:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg
1 5 10

10

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

20

(iii) HYPOTHETICAL: NO

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Ala Asn Xaa Tyr Tyr Glu Lys Ala Glu
1 5 10

30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

10

CANGCNTTNN NNCANTTNAC NTTNGANNG

29

(2) INFORMATION FOR SEQ ID NO:24:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

30

TCNGCNTTNT CNTANTANTT NTTNGC

26

(2) INFORMATION FOR SEQ ID NO:25:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5

(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TACAATCAGC TGATGACCAG AACGCTC

27

15

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